



Figure 1A

Compd #	MOLSTRUCTURE
1	
2	
3	
4	
5	
6	
7	

Figure 1B

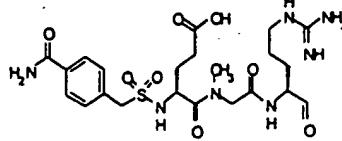
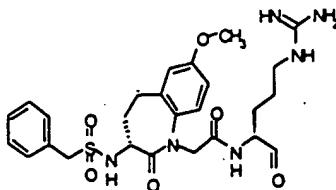
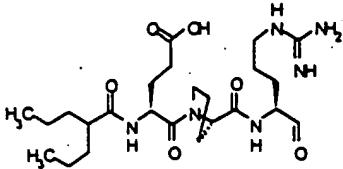
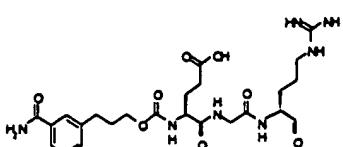
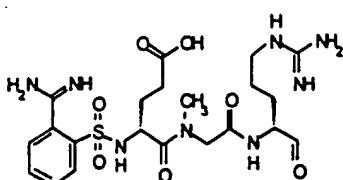
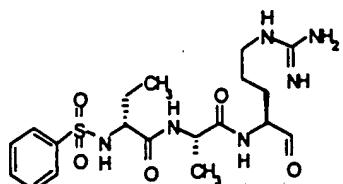
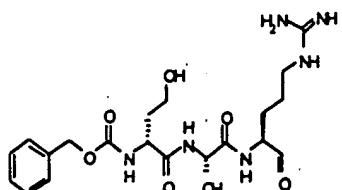
Compd #	MOLSTRUCTURE
8	
9	
10	
11	
12	
13	
14	

Figure 1C

Compd #	MOLSTRUCTURE	Compd #	MOLSTRUCTURE
15		20	
16		21	
17		22	
18		23	
19			

FIGURE 2A

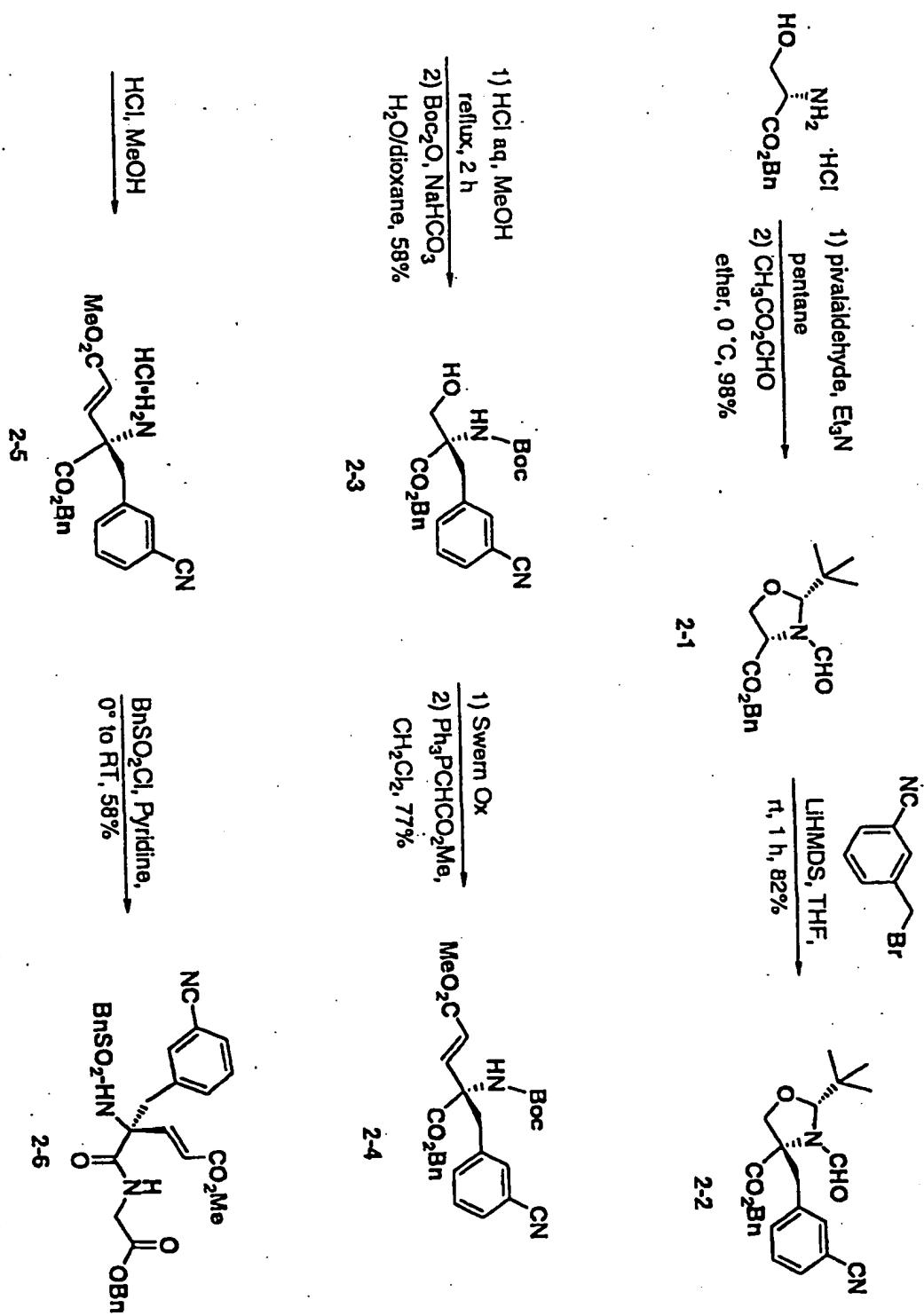
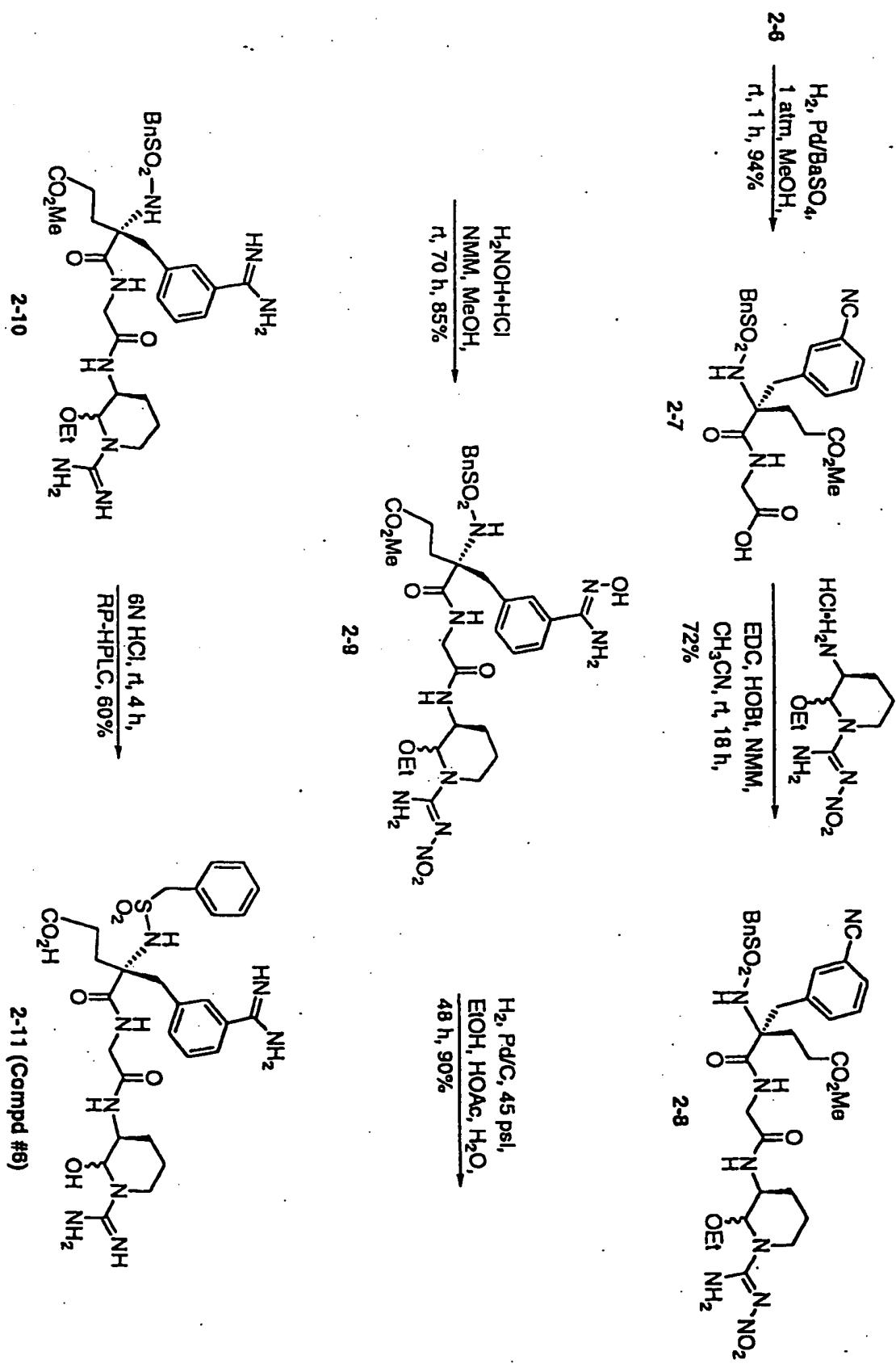


FIGURE 2B



## FIGURE 3A

10 20 30 40 50 60  
 GTTGGTGGGGCACGGATGGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCT  
 CAACAACCCCCGTGCCTACGCCTACTCCGCTCACCGGGACCGTCCATTGGACGTACGA  
 V V G G T D A D E G E W P W Q V S L H A>  
 70 80 90 100 110 120  
 CTGGGCCAGGGCACATCTCGGGTGTCTCCCTCATCTCTCCCAACTGGCTGGTCTCTGCC  
 GACCCGGTCCCGGTGTAGACGCCACGAAGGGAGTAGAGAGGGTTGACCGACCAAGACGG  
 L G Q G H I C G A S L I S P N W L V S A>  
 130 140 150 160 170 180  
 GCACACTGCTACATCGATGACAGAGGATTCAAGTACTCAGACCCCACGCAGTGGACGGCC  
 CGTGTGACGATGTAGCTACTGTCTCTAAGTCCATGAGTCTGGGTGCGTCACCTGCCGG  
 A H C Y I D D R G F R Y S D P T Q W T A>  
 190 200 210 220 230 240  
 TTCCCTGGCTTGACGACCAGAGCCAGCGCAGCGCCCTGGGTGCAGGAGCGCAGGCTC  
 AAGGACCCGAACGTGCTGGTCTCGGTGCGTGCAGGGACCCACGTCTCGGTCCGAG  
 F L G L H D Q S Q R S A P G V Q E R R L>  
 250 260 270 280 290 300  
 AAGCGCATCATCTCCACCCCTTCTCAATGACTTCACCTTCGACTATGACATCGCGCTG  
 TTGCGTAGTAGAGGGTGGGAAGAAGTTACTGAAGTGGAAAGCTGATACTGTAGCGCGAC  
 K R I I S H P F F N D F T F D Y D I A L>  
 310 320 330 340 350 360  
 CTGGAGCTGGAGAAACCGGCAGAGTACAGCTCATGGTGCAGGCCATCTGCCTGCCGGAC  
 GACCTCGACCTCTTGGCCGCTCATGTCGAGGTACCAACGCCGGTAGACGGACGGCTG  
 L E L E K P A E Y S S M V R P I C L P D>

FIGURE 3B

370            380            390            400            410            420  
 GCCTCCCATGTCTCCCTGCCGGCAAGGCCATCTGGGTACGGGCTGGGACACACCCAG  
 CGGAGGGTACAGAAGGGACGGCCGTTCCGGTAGACCCAGTGCCCACCCCTGTGTGGTC  
 A S H V F P A G K A I W V T G W G H T Q>  
  
 430            440            450            460            470            480  
 TATGGAGGCAGTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACC  
 ATACCTCCGTGACCGCGCGACTAGGACGTTTCCACTCTAGGCGCAGTAGTTGGTCTGG  
 Y G G T G A L I L Q K G E I R V I N Q T>  
  
 490            500            510            520            530            540  
 ACCTGCGAGAACCTCCTGCCGCAGCAGATCACGCCGCATGATGTGCGTGGGCTTCCTC  
 TGGACGCTCTGGAGGACGGCGTCGCTAGTGCAGCGCTACTACACGCACCCGAAGGAG  
 T C E N L L P Q Q I T P R M M C V G F L>  
  
 550            560            570            580            590            600  
 AGCGGGCGCGTGGACTCCTGCCAGGGTGATTCCGGGGACCCCTGTCCAGCGTGGAGGCG  
 TCGCCGCCGACCTGAGGACGGTCCCACTAAGGCCCCCTGGGACAGGTCGCACCTCCGC  
 S G G V D S C Q G D S G G P L S S V E A>  
  
 610            620            630            640            650            660  
 GATGGGCGGATCTTCAGGCCGGTGTGGTGAGCTGGGAGACGGCTGCCTCAGAGGAAC  
 CTACCCGCTAGAAGGTCCGGCCACACCACTCGACCCCTCTGCCGACGCGAGTCTCCTG  
 D G R I F Q A G V V S W G D G C A Q R N>  
  
 670            680            690            700            710            720  
 AAGCCAGGCCTGTACACAAGGCTCCCTGTGTTGGGACTGGATCAAAGAGAACACTGGG  
 TTGGTCCGCACATGTGTTCCGAGGGAGACAAAGCCCTGACCTAGTTCTTTGTGACCC  
 K P G V Y T R L P L F R D W I K E N T G>

FIGURE 3C

GTATAG

CATATC

V \* >